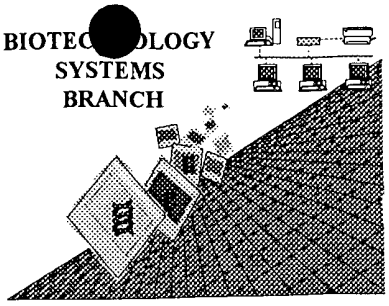
BIOTECHNOLOGY SYSTEMS BRANCH



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/673,395

Source: PCT 09

Date Processed by STIC: 1/23/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION SERIAL NUMBER: 09/673,395

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 ____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 ____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.

4 ____ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 ____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 ____ Variable Length
Sequence(s) ____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.

7 ____ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

8 ____ Skipped Sequences (OLD RULES)
Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 ____ Skipped Sequences (NEW RULES)
Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 ✓ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 ____ Use of <213>Organism (NEW RULES)
Sequence(s) _____ are missing this mandatory field or its response.

12 ____ Use of <220>Feature (NEW RULES)
Sequence(s) ____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)

13 ____ PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

PCT09

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/673,395

DATE: 01/23/2001
TIME: 11:53:49

Input Set : N:\COPIES\ES.txt
Output Set: N:\CRF3\01232001\I673395.raw

pp 1-4

Does Not Comply
Corrected Diskette Needed

do not use foreign accent marks; they do not translate in the CRF program

4 <110> APPLICANT: metaGen Gesellschaft für Genomforschung mbH (Assignee)
6 <120> TITLE OF INVENTION: Human Nucleic Acid Sequences from Uterus Tumor Tissue
8 <130> FILE REFERENCE: 51586AWOM1XX24-P
OK 10 <140> CURRENT APPLICATION NUMBER: US/09/673,395
OK 11 <141> CURRENT FILING DATE: 2000-10-17
13 <160> NUMBER OF SEQ ID NOS: 635

ERRORED SEQUENCES

14671 <210> SEQ ID NO: 494
14672 <211> LENGTH: 85 82 shows
14673 <212> TYPE: PRT
14674 <213> ORGANISM: homo sapiens
14676 <400> SEQUENCE: 494

14678	Lys	Gly	Ser	Leu	Pro	Pro	Thr	Lys	Gln	Gly	Lys	Leu	Gly	Gln	Leu	Ala
14679	1				5					10					15	
14681	Pro	Gly	His	Gln	Gly	Gln	Leu	Pro	Thr	Trp	Leu	Leu	Pro	Phe	Leu	Gly
14682				20					25					30		
14684	Phe	Phe	Gln	Gly	Phe	Gly	Asn	Ser	Leu	Gly	Val	Gly	Glu	Val	Ala	Ser
14685			35					40					45			
14687	Cys	Leu	His	Trp	Tyr	Trp	Pro	Arg	Arg	Trp	Ala	Gly	His	Gly	Gly	Gly
14688		50					55					60				
14690	Gly	Val	Asn	Ile	Trp	Phe	Ile	Ser	His	Pro	Ala	Gly	Cys	Lys	Pro	Leu
14691	65					70					75					80
E--> 14693	Val	Lys														

Please consult new sequence Rules for valid format.

17275 <210> SEQ ID NO: 573
17276 <211> LENGTH: 91
17277 <212> TYPE: PRT
17278 <213> ORGANISM: homo sapiens
17280 <400> SEQUENCE: 573

17282	Asp	Ser	Gln	Val	Gly	Arg	Gly	Pro	Gln	Arg	Asn	Ser	Ser	Leu	His	Thr
17283	1				5					10					15	
17285	Gly	Arg	Ser	Val	His	Trp	Gly	Glu	Ala	Thr	Gly	Ser	Leu	Arg	His	Leu
17286				20					25					30		
17288	Gln	Trp	Gly	Arg	Ala	Gln	Pro	Leu	Leu	Phe	Leu	Gly	Gly	Lys	Leu	Arg
17289			35					40					45			
E--> 17291	Phe	Lys	Leu	Pro	Gly	Gly	Lys	Ser	Met	Gly	Arg	Lys	Gln	Ala	Leu	Xxx
17292		50					55					60				
17294	Leu	Leu	Arg	Val	Ser	Val	Ser	Pro	Phe	Phe	Pro	Leu	Cys	Leu	Ile	Asn
17295	65					70					75					80
17297	Lys	Phe	His	Phe	Ser	His	Pro	Ser	Asn	Ser	Leu					
17298					85					90						

Per new sequence Rules, use Xaa AND explain in <2207-<2237 use Xaa section (see item 10 on Error Summary Sheet)

17300 <210> SEQ ID NO: 574
17301 <211> LENGTH: 89
17302 <212> TYPE: PRT
17303 <213> ORGANISM: homo sapiens

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/673,395

DATE: 01/23/2001
TIME: 11:53:53

Input Set : N:\COPIES\ES.txt
Output Set: N:\CRF3\01232001\I673395.raw

same error

17305 <400> SEQUENCE: 574

17307	Glu	Lys	Trp	Asn	Leu	Leu	Ile	Arg	His	Lys	Gly	Lys	Lys	Gly	Glu	Thr
17308	1				5					10					15	
E--> 17310	**Glu**	**Thr**	**Leu**	**Ser**	**Lys**	**Xxx**	**Arg**	**Ala**	**Cys**	**Phe**	**Leu**	**Pro**	**Met**	**Asp**	**Phe**	**Pro**
17311				20					25					30		
17313	Pro	Gly	Ser	Leu	Asn	Arg	Ser	Phe	Pro	Pro	Arg	Lys	Arg	Arg	Gly	Trp
17314			35					40					45			
17316	Ala	Leu	Pro	His	Trp	Arg	Trp	Arg	Lys	Leu	Pro	Val	Ala	Ser	Pro	Gln
17317		50					55					60				
17319	Cys	Thr	Leu	Leu	Pro	Val	Cys	Arg	Leu	Glu	Phe	Leu	Trp	Gly	Pro	Leu
17320	65					70					75					80
17322	Pro	Thr	Trp	Leu	Ser	His	Cys	Pro	Leu							
17323					85											

17351 <210> SEQ ID NO: 577
17352 <211> LENGTH: 161
17353 <212> TYPE: PRT
17354 <213> ORGANISM: homo sapiens
17356 <400> SEQUENCE: 577

E--> 17358	**Leu**	**Leu**	**Pro**	**Leu**	**Leu**	**Leu**	**Leu**	**Leu**	**Ile**	**His**	**Gly**	**Asp**	**Thr**	**Pro**	**Xxx**	**Gly**
17359	1				5					10					15	
E--> 17361	**Pro**	**Gly**	**Pro**	**Xxx**	**Xxx**	**Gln**	**Glu**	**Gln**	**Ala**	**Pro**	**Asn**	**His**	**Arg**	**His**	**Gly**	**Leu**
17362				20					25					30		
E--> 17364	**Glu**	**Glu**	**Xxx**	**Arg**	**Ile**	**Ser**	**Xxx**	**Lys**	**Ser**	**Cys**	**Met**	**Gly**	**Xxx**	**Val**	**Asp**	**Trp**
17365			35					40					45			
17367	Asn	Gly	Pro	Glu	Gly	Val	Glu	Ile	Tyr	Val	Asp	Gly	Lys	Glu	Pro	His
17368		50					55					60				
E--> 17370	**Asn**	**Lys**	**Ser**	**Gln**	**Ser**	**Ser**	**Gln**	**Leu**	**Gly**	**Phe**	**Lys**	**Thr**	**Asn**	**Gly**	**His**	**Xxx**
17371	65					70					75					80
E--> 17373	**Lys**	**Ser**	**Ser**	**Glu**	**Xxx**	**Val**	**Xxx**	**His**	**Asp**	**Val**	**Leu**	**Asp**	**Asn**	**Arg**	**Lys**	**Glu**
17374					85					90					95	
17376	Ala	Gly	Val	Lys	Val	Lys	Glu	Gly	His	Glu	His	Gln	Asn	Gln	Gln	Asp
17377				100					105					110		
17379	Pro	Ala	Ser	Glu	Leu	His	Val	Leu	Phe	Gly	Gly	Ala	Leu	Thr	His	Gly
17380			115					120					125			
17382	Gly	Asp	Ala	Arg	Lys	His	Ala	Leu	Pro	Phe	Arg	Thr	Gly	Phe	Ser	Arg
17383		130					135					140				
17385	Ser	Thr	Gln	Gln	Pro	Pro	Pro	Arg	Ala	Arg	Phe	Leu	Pro	Leu	Cys	Arg
17386	145					150					155					160
17388	Thr															

same

17390 <210> SEQ ID NO: 578
17391 <211> LENGTH: 160
17392 <212> TYPE: PRT
17393 <213> ORGANISM: homo sapiens
17395 <400> SEQUENCE: 578

E--> 17397	**Gln**	**Thr**	**Asp**	**Asn**	**Leu**	**Ser**	**Glu**	**Arg**	**Gln**	**Pro**	**Xxx**	**Gly**	**Lys**	**Xxx**	**Val**	**Cys**
17398	1				5					10					15	
17400	Arg	Gly	Cys	Pro	Gln	Gly	Glu	Cys	Ser	Trp	Glu	Arg	Ala	Val	Leu	Leu
17401				20					25					30		
E--> 17403	**Xxx**	**Pro**	**Gly**	**Arg**	**Pro**	**Ala**	**Leu**	**Ser**	**Xxx**	**Thr**	**Leu**	**Leu**	**Xxx**	**Lys**	**Xxx**	**Ala**

same

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/673,395

DATE: 01/23/2001
TIME: 11:53:53

Input Set : N:\COPIES\ES.txt
Output Set: N:\CRF3\01232001\I673395.raw

```
      17404                35                       40                       45
E--> 17406  Pro  Cys  Glu  Val  Asn  Trp  Val  Xxx  Val  Arg  Gly  Ser  Xxx  Xxx  Cys  Xxx
      17407       50                       55                       60
E--> 17409  Gly  Ala  Pro  Ala  Xxx  Thr  Pro  Xxx  Pro  Xxx  Gln  Arg  Xxx  Ala  Ala  Ser
      17410  65                       70                       75                       80
E--> 17412  Ala  Xxx  Ala  Gly  Leu  Glu  Xxx  Ser  Xxx  Ala  Xxx  Ala  Gly  Xxx  Ala  Gly
      17413                     85                       90                       95
E--> 17415  Cys  Cys  Cys  Xxx  Gly  Leu  Pro  Xxx  Val  Trp  Ser  Xxx  Leu  Ala  Leu  Pro
      17416                100                      105                      110
E--> 17418  Thr  Ala  Ser  Leu  Glu  Ala  Ser  Xxx  Xxx  Pro  Arg  Pro  Ala  Ala  Ser  Pro
      17419           115                      120                      125
      17421  Arg  Thr  Ser  Cys  Pro  Ser  Thr  Leu  Pro  Gln  Ala  Thr  Lys  Thr  Pro  Arg
      17422       130                      135                      140
E--> 17424  Val  Leu  Pro  Asn  Lys  Xxx  Xxx  Leu  Gly  Thr  Xxx  Ser  Lys  Leu  Ile  Phe
      17425  145                      150                      155                      160
      18471 <210> SEQ ID NO: 603
      18472 <211> LENGTH: 163
      18473 <212> TYPE: PRT
      18474 <213> ORGANISM: homo sapiens
      18476 <400> SEQUENCE: 603
      18478  Ile  Tyr  Gly  Val  Ser  Phe  Leu  Ile  Phe  Asn  Ile  Lys  Asn  Ile  Tyr  Val
      18479   1                   5                        10                       15
      18481  Ser  Val  Ile  Pro  Cys  Gln  Gly  Cys  Leu  Leu  Val  Cys  Leu  Arg  Phe  Cys
      18482                 20                       25                       30
      18484  Phe  Ile  Phe  Ile  His  Val  Val  Val  Ile  Phe  Ser  Ser  Gln  Phe  Leu  Leu
      18485            35                       40                       45
      18487  Val  Ser  Pro  Phe  Pro  Gly  Ser  Phe  Leu  Leu  Leu  Leu  Leu  Ser  Val  Gly
      18488       50                       55                       60
      18490  Asp  Asp  Lys  Leu  Val  Ser  Leu  Arg  Ala  Leu  His  Leu  Trp  Ile  Phe  Leu
      18491  65                       70                       75                       80
E--> 18493  Xxx  Ser  Leu  Thr  Gly  Gln  Pro  Ala  Pro  Val  Gly  Ser  Gly  Pro  Val  Leu
      18494                     85                       90                       95
E--> 18496  Arg  Leu  Pro  Arg  Ser  Leu  Phe  His  Leu  Gln  Val  Cys  Leu  Pro  Xxx  Pro
      18497                100                      105                      110
      18499  Ala  Pro  Gly  Leu  Ala  Pro  Ala  Ala  Ala  Cys  Pro  Ser  Glu  Ala  Leu  Leu
      18500           115                      120                      125
      18502  Ser  Pro  Pro  Gly  Ser  His  Gly  Trp  Phe  Pro  Leu  Ser  Gln  Leu  Val  Ser
      18503       130                      135                      140
      18505  Leu  Asn  Pro  Lys  Pro  Leu  Arg  Asn  Trp  Gly  Leu  Val  Ser  Gly  Thr  Cys
      18506  145                      150                      155                      160
      18508  Cys  Tyr  Gln
      18510 <210> SEQ ID NO: 604
      18511 <211> LENGTH: 150
      18512 <212> TYPE: PRT
      18513 <213> ORGANISM: homo sapiens
      18515 <400> SEQUENCE: 604
      18517  Pro  Leu  Ser  Phe  Leu  Met  Tyr  Lys  Thr  Leu  Leu  Ser  Gly  Leu  Glu  Phe
      18518   1                   5                        10                       15
E--> 18520  Glu  His  Leu  Trp  Xxx  Phe  Ile  Tyr  Phe  Ala  Xxx  Val  Cys  Gly  Gln  Ser
```

same

same

same

```
                    RAW SEQUENCE LISTING                        DATE: 01/23/2001
                    PATENT APPLICATION:  US/09/673,395          TIME: 11:53:53

                    Input Set : N:\COPIES\ES.txt
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       18521                         20                   25                  30
E--> 18523  Asn  Ile  Phe  Pro  Lys  Tyr  Ile  Leu  Pro  Arg  Lys  Xxx  Lys  Lys  Gln  Ile
       18524                 35                  40                       45
E--> 18526  Arg  Xxx  Phe  Asp  Xxx  Lys  Xxx  Asn  Arg  Pro  Xxx  Lys  Gly  Ala  Xxx  Thr
       18527        50                      55                        60
E--> 18529  Trp  Ser  Arg  Ala  Trp  Xxx  Arg  Gly  Lys  Ala  Xxx  Arg  Gly  Gln  Val  Cys
       18530   65                      70                       75                       80
E--> 18532  Cys  Gly  Gln  Ile  Cys  Ala  Tyr  Phe  Ile  Thr  Gly  Val  Lys  Xxx  Lys  Gln
       18533                     85                  90                            95
E--> 18535  Ser  Xxx  Ile  Asp  Val  Xxx  Arg  Ile  Tyr  Thr  Val  Xxx  Arg  Asn  Xxx  Arg
       18536               100                      105                       110
E--> 18538  Xxx  Xxx  Phe  Xxx  Lys  Asn  Arg  Asn  Thr  Xxx  Trp  Xxx  Xxx  Phe  Tyr  His
       18539       115                      120                      125
E--> 18541  Xxx  Xxx  Tyr  Thr  Phe  Ser  Leu  Trp  Xxx  Asn  Xxx  Leu  Thr  Lys  Leu  Xxx
       18542       130                      135                      140
       18544  Phe  Lys  Ile  Lys  Leu  Met
       18545  145                      150
       19593 <210> SEQ ID NO: 635
       19594 <211> LENGTH: 89
       19595 <212> TYPE: PRT
       19596 <213> ORGANISM: homo sapiens
       19598 <400> SEQUENCE: 635
       19600  Phe  Ile  Gln  Phe  Ser  Arg  Pro  Gly  Ser  Pro  Leu  Ser  Leu  Asp  Gly  Leu
       19601   1                   5                   10                  15
E--> 19603  Ser  Xxx  Ala  Ile  Ala  Ser  Cys  Xxx  Leu  Asn  His  Thr  Ala  Asn  Pro  Thr
       19604                 20                       25                  30
       19606  Ser  Asn  Ser  Asn  Phe  Leu  Asp  Leu  Asn  Leu  Pro  Pro  Gln  His  Asn  Thr
       19607            35                       40                       45
       19609  Gly  Leu  Gly  Gly  Ile  Pro  Val  Ala  Gly  Glu  Glu  Glu  Val  Lys  Val  Ser
       19610       50                       55                       60
       19612  Thr  Met  Pro  Leu  Ser  Thr  Ser  Ser  His  Ser  Leu  Gln  Gln  Gly  Gln  Gln
       19613   65                      70                       75                       80
       19615  Pro  Thr  Ser  Leu  His  Thr  Thr  Val  Ala
       19616                     85
E--> 19626 276
E--> 19629 265
E--> 19632 295
E--> 19635 312
```

same

same

delete at end of file

FYI

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/673,395

DATE: 01/23/2001
TIME: 11:53:54

Input Set : N:\COPIES\ES.txt
Output Set: N:\CRF3\01232001\I673395.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:2151 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:79
L:2151 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:79
L:2151 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:79
L:11033 M:283 W: Missing Blank Line separator, <400> field identifier
L:11034 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (359) SEQUENCE:
L:14693 M:252 E: No. of Seq. differs, <211>LENGTH:Input:83 Found:82 SEQ:494
L:15633 M:283 W: Missing Blank Line separator, <400> field identifier
L:15634 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (529) SEQUENCE:
L:15637 M:283 W: Missing Blank Line separator, <400> field identifier
L:15638 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (530) SEQUENCE:
L:15812 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:535
L:15812 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:535
L:15812 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:535
L:15812 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:535
L:15812 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:535
L:15816 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:535
L:15816 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:535
L:15816 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:535
L:15816 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:535
M:340 Repeated in SeqNo-535
L:15839 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:536
L:15839 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:536
L:15839 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:536
L:15839 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:536
L:15839 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:536
L:15840 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:536
L:15840 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:536
L:15840 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:536
L:15840 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:536
M:340 Repeated in SeqNo=536
L:15841 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:536
L:15841 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:536
L:15841 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:536
L:15841 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:536
L:15842 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:536
L:15842 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:536
L:15842 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:536
L:15842 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:536
L:15843 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:536
L:15843 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:536
L:15843 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:536
L:15843 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:536
L:15844 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:536
L:15844 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:536
L:15844 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:536
L:15844 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:536

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/673,395

DATE: 01/23/2001
TIME: 11:53:54

Input Set : N:\COPIES\ES.txt
Output Set: N:\CRF3\01232001\I673395.raw

L:15845 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:536
L:15845 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:536
L:15845 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:536
L:15845 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:536
L:15846 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:536
L:15846 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:536
L:15846 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:536
L:15846 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:536
L:15847 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:536
L:15847 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:536
L:15847 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:536
L:15847 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:536
L:15848 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:536
L:15848 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:536
L:15848 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:536
L:15848 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:536
L:16273 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:545
M:340 Repeated in SeqNo=545
L:16488 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:550
M:340 Repeated in SeqNo=550
L:16573 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:552
M:340 Repeated in SeqNo=552
L:16604 M:283 W: Missing Blank Line separator, <400> field identifier
L:16605 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (553) SEQUENCE:
L:16654 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:555
L:16663 M:283 W: Missing Blank Line separator, <400> field identifier
L:16664 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (556) SEQUENCE:
L:16667 M:283 W: Missing Blank Line separator, <400> field identifier
L:16668 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (557) SEQUENCE:
L:16671 M:283 W: Missing Blank Line separator, <400> field identifier
L:16672 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (558) SEQUENCE:
L:16675 M:283 W: Missing Blank Line separator, <400> field identifier
L:16676 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (559) SEQUENCE:
L:16679 M:283 W: Missing Blank Line separator, <400> field identifier
L:16680 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (560) SEQUENCE:
L:17291 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:17310 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:17348 M:283 W: Missing Blank Line separator, <400> field identifier
L:17349 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (576) SEQUENCE:
L:17358 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:17361 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:17364 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
L:17370 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:17373 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:17397 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:17403 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:4
L:17406 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:4
L:17409 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:4
L:17412 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:5

VERIFICATION SUMMARY DATE: 01/23/2001
PATENT APPLICATION: US/09/673,395 TIME: 11:53:54

Input Set : N:\COPIES\ES.txt
Output Set: N:\CRF3\01232001\I673395.raw

L:17415 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
L:17418 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:17424 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
L:18493 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:18496 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:18520 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:18523 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:18526 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:5
L:18529 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:18532 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:18535 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:4
L:18538 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:6
L:18541 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:5
L:18554 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:18557 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:6
L:18560 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:4
L:18563 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:18566 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:18569 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:6
L:18572 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:19049 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:19052 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:19058 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:19061 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:19067 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:19079 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:19089 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:19165 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:19168 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:19174 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:19177 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:19180 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:19183 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:19367 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:19407 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:19419 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:19423 M:283 W: Missing Blank Line separator, <400> field identifier
L:19424 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (626) SEQUENCE:
L:19427 M:283 W: Missing Blank Line separator, <400> field identifier
L:19428 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (627) SEQUENCE:
L:19431 M:283 W: Missing Blank Line separator, <400> field identifier
L:19432 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (628) SEQUENCE:
L:19435 M:283 W: Missing Blank Line separator, <400> field identifier
L:19436 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (629) SEQUENCE:
L:19562 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:19565 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:19626 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:635
M:332 Repeated in SeqNo=635